REMARKS

I. Support for Amendments

The specification was amended in order to correct typographical errors. Specifically, the paragraphs beginning on page 6, line 27 and page 7, line 10, were amended in order to correct a typographical error regarding the appropriate amino acid residues of the hZP3 protein. These paragraphs should refer to residues "308 to 348" as opposed to "308 to 349". This amendment is supported by the description of Figures 1 and 2 on page 6, which state that these Figures depict residues 308 to 348 of human ZP3. Furthermore, this amendment is also supported by page 8, line 11 of the specification which states, "Another aspect of the invention is that the amino acid sequences within residues 308 to 348 of ZP3 effects and directs human specific oocyte glycosylation, being species specific."

The paragraph beginning on page 19, line 27 was also corrected in order to correct a typographical error regarding the molecular weight of hZP3. The correct molecular weight is 47kd. This amendment is supported by the fact that 47kd was initially recited in the specification except for the typographical error in which "kd" was recited as "kb."

A substitute Sequence Listing is being submitted to correct errors in the hZP3 protein sequence designated as SEQ ID. NOS. 1 and 2 (which are identical sequences). The corrected sequences are fully supported by the application as originally filed and, as explained below, do not present new matter.

In particular, the previous SEQ ID NOS: 1 and 2 were both incorrect as SEQ ID NO: 1 contained errors at four amino acid residues while SEQ ID NO: 2 contained errors at two amino

acid residues. In an amendment dated February 28, 2001, it was applicants' belief that SEQ ID NO: 1 was incorrect in that it omitted a Cys residue at the 327 position and recited a Glu instead of a Gln residue at the 336 position. It was applicants further belief that SEQ ID NO: 2 was the correct sequence for hZP3 and, therefore, all citations to SEQ ID NO: 1 were amended to refer to SEQ ID NO: 2 instead. However, applicants are now informed and believe that the amino acid sequence recited in SEQ ID NO: 2 is also incorrect. The amino acid sequence of SEQ ID NO: 2 contains two errors in that it recites a Gln residue at position 313 and a Val residue at position 347. The correct sequence, as found in Chamberlin and Dean, *Proc. Nat. Acad. Sci. U.S.A.* 87: 6014-6018 (1990) in Figure 3 on page 6017 (a copy of which is included), should recite a **Glu** residue at position 313 and an **Ala** residue at position 347. This sequence difference appears to have arisen as an inadvertent error and does not represent new matter as those of skill in the art would be aware that the correct human ZP3 sequence was already known in the prior art as referenced in the specification and exemplified in the Chamberlin reference.[1]

Support for this amended sequence is found throughout the specification. For instance, as noted on page 3, lines 2-4, and page 13, lines 11-13, the ZP3 protein was characterized by Chamberlin and Dean in 1990. Furthermore, Example 2 on page 19 of the specification, which discusses the cloning of the human ZP3 into the expression vector, states on lines 27-28, "DNA sequence analysis of hZP3 cDNA revealed that the hZP3 cDNA sequence is identical to that published by Chamberlin and Dean, *Proc. Nat. Acad. Sci. U.S.A.* 87: 6014-6018 (1990)." In addition, as stated on page 6 of the specification, Figure 1 is identified as "residues 308 to 348 of

[1] Although the Chamberlin reference does cite the known hZP3 amino acid sequence, it does not identify the necessity for proper glycosylation of the peptides recited in the instant application.

human ZP3" while Figure 2 depicts the "prediction summary of O-glycosylation sites on the 308-348 amino acid region of human ZP3."

Claims 73-74 and Figures 1-2 have also been amended in order to correct the typographical errors in the ZP3 amino acid sequence as explained above. Specifically, the ZP3 sequence shown in claims 73-74 and Figures 1-2 contain the same two errors as the ones recited in SEQ ID NO: 2. Claims 69 and 71 were amended in order to more clearly define the invention. Support for this amendment is found throughout the specification, for example, on page 7, lines 18-21, lines 25-26, page 18, lines 5-13, and pages 19-23. Accordingly, no new matter is added by this Amendment and entry thereof is respectfully requested.

II. ARGUMENTS CONCERNING OUTSTANDING REJECTIONS

Applicants contend that, while the sequence information was inadvertently incorrect, the arguments presented in the Amendment filed October 3, 2003 are pertinent. With regard to the rejection of previously canceled claims 48-68 under 35 U.S.C. § 112, first paragraph, we submit that currently amended claims 69, 71, 73-74, and claims 70, 72, and 78 (containing amended SEQ ID NO: 2), are sufficiently supported in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors had possession of the claimed invention. The specification provides a detailed description of the recombinantly produced polypeptide and glycopolypeptide of SEQ ID NO: 2 and conservative amino acid substitutions thereof, and teaches a properly glycosylated recombinant human ZP3 protein expressed by a human ovarian cell line. Therefore, amended claims 69-74, and 78 are adequately described in

the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the claimed invention.

Furthermore, with regard to the rejection of previously canceled claims 48-56 and 60-68 under 35 U.S.C. § 102(b) and (e) as being anticipated by Dean (U.S. Patent No. 5,641,487) and Dean (U.S. Patent No. 5,672,488), applicants submit that newly amended claims 69-74, and 78 are not anticipated by Dean. Specifically, Dean does not teach the recombinantly produced polypeptide of SEQ ID NO: 2, the recombinantly produced polypeptide of SEQ ID NO: 2 having the amino acid substitutions of claims 71-74, or the expression of hZP3 by a human ovarian cell line. Hence, Dean does not teach every element of claim 69-74, and 78, and, therefore, does not anticipate these claims.

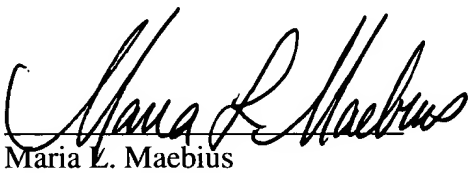
Similarly, with regard to the rejection of previously canceled claims 57-59 under 35 U.S.C. § 103(a) as being unpatentable over Dean (U.S. Patent No. 5,641,487) or Dean (U.S. Patent No. 5,672,488) in view of Chamberlin et al. (Proc.Natl.Acad.Sci. USA, Developmental Biology, Vol. 87, pp. 6014-6018, August 1990) and in further view of Stern et al. (U.S. Patent No. 5,869,053), applicants submit that newly amended claims 69-74 and 78 are not obvious over the Dean, Chamberlin, and Stern references. Chamberlin and Stern do not describe the claimed polypeptides and, therefore, do not remedy the deficiencies of the Dean patents described above.

Therefore, applicants respectfully request that the previous rejections be withdrawn.

III. CONCLUSION

In view of the foregoing remarks, Applicants believe that the application is in condition for allowance. However, if the Examiner disagrees, she is encouraged to call the undersigned at the number listed below in order to expedite the prosecution of this application.

Respectfully submitted,



Maria L. Maebius
Attorney for Applicant
Reg. No. 42,967

Date: 18 May 2004

Hale and Dorr LLP
1455 Pennsylvania Ave., NW
Washington, D.C. 20004
(202) 942-8452

Annotated Sheet Showing Changes

Figure 1

Glu
Ser Trp Phe Pro Val ~~Gln~~ Gly Pro Ala Asp Ile Cys Gln Cys Cys Asn Lys Gly Asp Cys Gly
308 318 328

Ala
Thr Pro Ser His Ser Arg Arg Gln Pro His Val Met Ser Gln Trp Ser Arg Ser ~~Val~~ Ser (SEQ ID NO: 2)
338 348

Annotated Sheet Showing Changes

Figure 2

Name: E HUMAN Length: 41

SWFPV~~Q~~GPADICQCCNKGDCGTPSHSRRQPHVMSQWSRS~~V~~A~~S~~ (SEQ ID NO: 2)

Name	Residue	No.	Potential	Threshold	Assignment
HUMAN	Thr	22	0.0285	0.4982	

Name	Residue	No.	Potential	Threshold	Assignment
HUMAN	Ser	1	0.0629	0.5132	
HUMAN	Ser	24	0.0104	0.5253	
HUMAN	Ser	26	0.0265	0.5309	
HUMAN	Ser	34	0.0033	0.6267	
HUMAN	Ser	37	0.4498	0.5825	
HUMAN	Ser	39	0.0009	0.5126	
HUMAN	Ser	41	0.0082	0.5022	